



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

Source

Date Processed by STIC:

10/797,248
IFW0
3/22/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses

1. EFS-Bio (<<http://www.uspto.gov/ehc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313 1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03



IFWO

RAW SEQUENCE LISTING

DATE: 03/22/2004

PATENT APPLICATION: US/10/797,248

TIME: 09:34:26

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J797248.raw

3 <110> APPLICANT: Dumas, Renaud
 4 Lebrun, Marc-Henri
 5 Zundel, Jean-Luc
 6 Effantin, G,raldine
 7 Morin, Val,rie
 9 <120> TITLE OF INVENTION: Use of inhibitors of ketol-acid reductoisomerase to prevent
 or treat
 10 fungal infection of plants
 12 <130> FILE REFERENCE: A36156-PCT-USA-A 072667.0196
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/797,248
 C--> 15 <141> CURRENT FILING DATE: 2004-03-10
 17 <160> NUMBER OF SEQ ID NOS: 18
 19 <170> SOFTWARE: Custom
 21 <210> SEQ ID NO: 1
 22 <211> LENGTH: 402
 23 <212> TYPE: PRT
 24 <213> ORGANISM: Magnaporthe grisea
 26 <220> FEATURE:
 27 <221> NAME/KEY: TRANSIT
 28 <222> LOCATION: (1)..(51)
 29 <223> OTHER INFORMATION: Putative mitochondrial transit peptide
 31 <400> SEQUENCE: 1
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 33 1 5 10 15
 35 Leu Ala Thr Pro Ala Val Gln Arg Arg Ser Phe Val Ala Ala Ser Ser
 36 20 25 30
 38 Met Val Arg Ala Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln
 39 35 40 45
 41 Ile Arg Gly Val Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val
 42 50 55 60
 44 Trp Glu Arg Ala Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys
 45 65 70 75 80
 47 Asp Asp Thr Leu Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln
 48 85 90 95
 50 Gly Leu Asn Leu Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg
 51 100 105 110
 53 Lys Asp Gly Lys Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro
 54 115 120 125
 56 Gly Lys Asn Leu Phe Glu Val Asp Glu Ala Ile Ser Arg Gly Thr Val
 57 130 135 140
 59 Ile Met Asn Leu Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala
 60 145 150 155 160
 62 Leu Lys Pro Gln Ile Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly
 63 165 170 175

pg. 6
 Does Not Comply
 Corrected Diskette Needed
 (B 7-9)

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Input Set : A:\PTO.DA.txt

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65 Phe Ser Pro Val Phe Lys Asp Leu Thr Lys Val Glu Val Pro Thr Asp
66      180      185      190
68 Val Asp Val Ile Leu Cys Ala Pro Lys Gly Ser Gly Arg Thr Val Arg
69      195      200      205
71 Ser Leu Phe Arg Glu Gly Arg Gly Ile Asn Ser Ser Phe Ala Val Tyr
72      210      215      220
74 Gln Asp Val Thr Gly Glu Ala Glu Glu Lys Ala Ile Ala Leu Gly Val
75 225      230      235      240
77 Ala Ile Gly Ser Gly Tyr Leu Tyr Lys Thr Thr Phe Glu Lys Glu Val
78      245      250      255
80 Tyr Ser Asp Leu Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His
81      260      265      270
83 Gly Met Phe Leu Ala Gln Tyr Glu Val Leu Arg Glu Arg Gly His Ser
84      275      280      285
86 Pro Ser Glu Ala Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu
87      290      295      300
89 Tyr Pro Leu Ile Gly Ala Asn Gly Met Asp Trp Met Tyr Glu Ala Cys
90 305      310      315      320
92 Ser Thr Thr Ala Arg Arg Gly Ala Ile Asp Trp Ser Pro Arg Phe Lys
93      325      330      335
95 Asp Ala Leu Lys Pro Val Phe Asn Gln Leu Tyr Asp Ser Val Lys Asp
96      340      345      350
98 Gly Ser Glu Thr Gln Arg Ser Leu Asp Tyr Asn Ser Gln Pro Asp Tyr
99      355      360      365
101 Arg Glu Lys Tyr Glu Ala Glu Met Glu Glu Ile Arg Asn Leu Glu Ile
102      370      375      380
104 Trp Arg Ala Gly Lys Ala Val Arg Ser Leu Arg Pro Glu Asn Gln Lys
105 385      390      395      400
107 Gln Lys
111 <210> SEQ ID NO: 2
112 <211> LENGTH: 395
113 <212> TYPE: PRT
114 <213> ORGANISM: Saccharomyces cerevisiae
116 <220> FEATURE:
117 <221> NAME/KEY: TRANSIT
118 <222> LOCATION: (1)..(47)
119 <223> OTHER INFORMATION: mitochondrial transit peptide
121 <300> PUBLICATION INFORMATION:
122 <308> DATABASE ACCESSION NO: gb:X04969
123 <309> DATABASE ENTRY DATE: 1993-09-12
125 <400> SEQUENCE: 2
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127 1      5      10      15
130 Thr Ala Lys Arg Thr Phe Ala Leu Ala Thr Arg Ala Ala Ala Tyr Ser
131      20      25      30
133 Arg Pro Ala Ala Arg Phe Val Lys Pro Met Ile Thr Thr Arg Gly Leu
134      35      40      45
136 Lys Gln Ile Asn Phe Gly Gly Thr Val Glu Thr Val Tyr Glu Arg Ala
137      50      55      60

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139 Asp Trp Pro Arg Glu Lys Leu Leu Asp Tyr Phe Lys Asn Asp Thr Phe
140 65 70 75 80
142 Ala Leu Ile Gly Tyr Gly Ser Gln Gly Tyr Gly Gln Gly Leu Asn Leu
143 85 90 95
145 Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Ala
146 100 105 110
148 Ser Trp Lys Ala Ala Ile Glu Asp Gly Trp Val Pro Gly Lys Asn Leu
149 115 120 125
151 Phe Thr Val Glu Asp Ala Ile Lys Arg Gly Ser Tyr Val Met Asn Leu
152 130 135 140
154 Leu Ser Asp Ala Ala Gln Ser Glu Thr Trp Pro Ala Ile Lys Pro Leu
155 145 150 155 160
157 Leu Thr Lys Gly Lys Thr Leu Tyr Phe Ser His Gly Phe Ser Pro Val
158 165 170 175
160 Phe Lys Asp Leu Thr His Val Glu Pro Pro Lys Asp Leu Asp Val Ile
161 180 185 190
163 Leu Val Ala Pro Lys Gly Ser Gly Arg Thr Val Arg Ser Leu Phe Lys
164 195 200 205
166 Glu Gly Arg Gly Ile Asn Ser Ser Tyr Ala Val Trp Asn Asp Val Thr
167 210 215 220
169 Gly Lys Ala His Glu Lys Ala Gln Ala Leu Ala Val Ala Ile Gly Ser
170 225 230 235 240
172 Gly Tyr Val Tyr Gln Thr Thr Phe Glu Arg Glu Val Asn Ser Asp Leu
173 245 250 255
175 Tyr Gly Glu Arg Gly Cys Leu Met Gly Gly Ile His Gly Met Phe Leu
176 260 265 270
178 Ala Gln Tyr Asp Val Leu Arg Glu Asn Gly His Ser Pro Ser Glu Ala
179 275 280 285
181 Phe Asn Glu Thr Val Glu Glu Ala Thr Gln Ser Leu Tyr Pro Leu Ile
182 290 295 300
184 Gly Lys Tyr Gly Met Asp Tyr Met Tyr Asp Ala Cys Ser Thr Thr Ala
185 305 310 315 320
187 Arg Arg Gly Ala Leu Asp Trp Tyr Pro Ile Phe Lys Asn Ala Leu Lys
188 325 330 335
190 Pro Val Phe Gln Asp Leu Tyr Glu Ser Thr Lys Asn Gly Thr Glu Thr
191 340 345 350
193 Lys Arg Ser Leu Glu Phe Asn Ser Gln Pro Asp Tyr Arg Glu Lys Leu
194 355 360 365
196 Glu Lys Glu Leu Asp Thr Ile Arg Asn Met Glu Ile Trp Lys Val Gly
197 370 375 380
199 Lys Glu Val Arg Lys Leu Arg Pro Glu Asn Gln
200 385 390 395

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203 <210> SEQ ID NO: 3

204 <211> LENGTH: 400

205 <212> TYPE: PRT

206 <213> ORGANISM: Neurospora crassa

208 <220> FEATURE:

209 <221> NAME/KEY: TRANSIT

210 <222> LOCATION: (1)..(53)

RAW SEQUENCE LISTING

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211 <223> OTHER INFORMATION: putative mitochondrial transit peptide
 213 <300> PUBLICATION INFORMATION:
 214 <308> DATABASE ACCESSION NO: gb:M84189.1
 215 <309> DATABASE ENTRY DATE: 1996-05-23
 217 <400> SEQUENCE: 3

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219	1				5					10					15	
221	Leu	Ala	Thr	Pro	Ala	Val	Gln	Arg	Arg	Thr	Phe	Val	Ala	Ala	Ala	Ser
222				20					25					30		
224	Ala	Val	Arg	Ala	Ser	Val	Ala	Val	Lys	Ala	Val	Ala	Ala	Pro	Ala	Arg
225			35						40				45			
227	Gln	Gln	Val	Arg	Gly	Val	Lys	Thr	Met	Asp	Phe	Ala	Gly	His	Lys	Glu
228		50					55				60					
230	Glu	Val	His	Glu	Arg	Ala	Asp	Trp	Pro	Ala	Glu	Lys	Leu	Leu	Asp	Tyr
231	65					70					75				80	
233	Phe	Lys	Asn	Asp	Thr	Leu	Ala	Leu	Ile	Gly	Tyr	Gly	Ser	Gln	Gly	His
234					85					90				95		
236	Gly	Gln	Gly	Leu	Asn	Leu	Arg	Asp	Asn	Gly	Leu	Asn	Val	Ile	Val	Gly
237				100					105					110		
239	Val	Arg	Lys	Asn	Gly	Lys	Ser	Trp	Glu	Asp	Ala	Ile	Gln	Asp	Gly	Trp
240			115					120					125			
242	Val	Pro	Gly	Lys	Asn	Leu	Phe	Asp	Val	Asp	Glu	Ala	Ile	Ser	Arg	Gly
243		130					135					140				
245	Thr	Ile	Val	Met	Asn	Leu	Leu	Ser	Asp	Ala	Ala	Gln	Ser	Glu	Thr	Trp
246	145					150					155				160	
248	Pro	His	Ile	Lys	Pro	Gln	Ile	Thr	Lys	Gly	Lys	Thr	Leu	Tyr	Phe	Ser
249				165						170					175	
251	His	Gly	Phe	Ser	Pro	Val	Phe	Lys	Asp	Leu	Thr	Lys	Val	Glu	Val	Pro
252				180					185					190		
254	Thr	Asp	Val	Asp	Val	Ile	Leu	Val	Ala	Pro	Lys	Gly	Ser	Gly	Arg	Thr
255			195					200					205			
257	Val	Arg	Ser	Leu	Phe	Arg	Glu	Gly	Arg	Gly	Ile	Asn	Ser	Ser	Phe	Ala
258		210					215					220				
260	Val	Tyr	Gln	Asp	Val	Thr	Gly	Lys	Ala	Lys	Glu	Lys	Ala	Val	Ala	Leu
261	225					230					235				240	
263	Gly	Val	Ala	Val	Gly	Ser	Gly	Tyr	Leu	Tyr	Glu	Thr	Thr	Phe	Glu	Lys
264				245						250				255		
266	Glu	Val	Tyr	Ser	Asp	Leu	Tyr	Gly	Glu	Arg	Gly	Cys	Leu	Met	Gly	Gly
267				260					265					270		
269	Ile	His	Gly	Met	Phe	Leu	Ala	Gln	Tyr	Glu	Val	Leu	Arg	Glu	Arg	Gly
270			275					280					285			
272	His	Ser	Pro	Ser	Glu	Ala	Phe	Asn	Glu	Thr	Val	Glu	Glu	Ala	Thr	Gln
273			290				295						300			
275	Ser	Leu	Tyr	Pro	Leu	Ile	Gly	Ala	His	Gly	Met	Asp	Trp	Met	Phe	Asp
276	305					310					315				320	
278	Ala	Cys	Ser	Thr	Thr	Ala	Arg	Arg	Gly	Ala	Ile	Asp	Trp	Thr	Pro	Lys
279				325						330					335	
281	Phe	Lys	Asp	Ala	Leu	Lys	Pro	Val	Phe	Asn	Asn	Leu	Tyr	Asp	Ser	Val
282				340						345				350		

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284 Lys Asn Gly Asp Glu Arg Lys Arg Ser Leu Glu Tyr Asn Ser Gln Pro
285           355           360           365
287 Asp Tyr Arg Glu Arg Tyr Glu Ala Glu Leu Asp Glu Ile Arg Asn Leu
288       370           375           380
290 Glu Ile Trp Arg Ala Gly Lys Arg Ser Leu Arg Pro Glu Asn Gln Lys
291 385           390           395           400
297 <210> SEQ ID NO: 4
298 <211> LENGTH: 1356
299 <212> TYPE: DNA
300 <213> ORGANISM: Magnaporthe grisea
302 <220> FEATURE:
303 <221> NAME/KEY: 5'UTR
304 <222> LOCATION: (1)..(43)
306 <220> FEATURE:
307 <221> NAME/KEY: CDS
308 <222> LOCATION: (44)..(1246)
310 <220> FEATURE:
311 <221> NAME/KEY: 3'UTR
312 <222> LOCATION: (1247)..(1356)
314 <220> FEATURE:
315 <221> NAME/KEY: polyA_site
316 <222> LOCATION: (1322)..(1330)
318 <400> SEQUENCE: 4
319 ttgttttttct tggtttcctta ttctaccttg tcacacaaca aac atg tct gct cgc      55
320                                     Met Ser Ala Arg
321                                     1
323 ggt ttc tca aag gct ttg agg cca atg gcc cgc caa ttg gcc act ccc      103
324 Gly Phe Ser Lys Ala Leu Arg Pro Met Ala Arg Gln Leu Ala Thr Pro
325   5           10           15           20
327 gcc gtt cag agg cgt acc ttc gtg gct gct tct agc atg gtg cgg gcc      151
328 Ala Val Gln Arg Arg Thr Phe Val Ala Ala Ser Ser Met Val Arg Ala
329           25           30           35
331 acc agg aaa gcc gcc gtc gct ccc act cag cag cag atc cgt ggt gtc      199
332 Thr Arg Lys Ala Ala Val Ala Pro Thr Gln Gln Gln Ile Arg Gly Val
333           40           45           50
335 aag acc atg gat ttt gct ggc cac aag gag cag gtc tgg gag cgt gcc      247
336 Lys Thr Met Asp Phe Ala Gly His Lys Glu Gln Val Trp Glu Arg Ala
337       55           60           65
339 gac tgg ccc aag gag aag ctg ctg gag tac ttc aag gac gac acc ctt      295
340 Asp Trp Pro Lys Glu Lys Leu Leu Glu Tyr Phe Lys Asp Asp Thr Leu
341       70           75           80
343 gcc ctc atc ggc tat ggt tcg cag ggc cac ggc cag ggt ctt aac ctc      343
344 Ala Leu Ile Gly Tyr Gly Ser Gln Gly His Gly Gln Gly Leu Asn Leu
345   85           90           95           100
347 cgc gac aac ggc ctc aac gtc atc atc ggt gtg cgc aag gac gga aag      391
348 Arg Asp Asn Gly Leu Asn Val Ile Ile Gly Val Arg Lys Asp Gly Lys
349           105           110           115
351 tcg tgg aag gac gcc gtc cag gac ggc tgg gtt ccc ggc aag aac ctc      439
352 Ser Trp Lys Asp Ala Val Gln Asp Gly Trp Val Pro Gly Lys Asn Leu

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RAW SEQUENCE LISTING ERROR SUMMARY

DATE: 03/22/2004

PATENT APPLICATION: US/10/797,248

TIME: 09:34:27

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J797248.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:8; N Pos. 9,12

Seq#:9; N Pos. 6,12,15,18

Seq#:10; N Pos. 6,9,18

VARIABLE LOCATION SUMMARY

PATENT APPLICATION: US/10/797,248

DATE: 03/22/2004

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Use of n's or Xaa's (NEW RULES): *Error EXPLANATION: E*
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
in <220> to <223> section, please explain location of n or Xaa, and which
residue n or Xaa represents.

Seq#:8; N Pos. 9,12

Seq#:9; N Pos. 6,12,15,18

Seq#:10; N Pos. 6,9,18

10/797,248

Page 8 of 9

<210> SEQ ID NO 8
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the artificial sequence: primer 2
<400> SEQUENCE: 8
atgtt~~yy~~ng dncartayga

please explain
"N" locations and
which location
"N"
Represents.

<210> SEQ ID NO 9
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the artificial sequence: primer 3
<400> SEQUENCE: 9
gayg~~nt~~ggg tnc~~ong~~naa

← please explain,
Same error

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<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of the artificial sequence: primer 4
<400> SEQUENCE: 10
atgg~~g~~gna tacaygg~~at~~ g

← please explain,
Same error

↑ Please see error
explanation on
page 7.

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/797,248

DATE: 03/22/2004

TIME: 09:34:27

Input Set : A:\PTO.DA.txt

Output Set: N:\CRF4\03222004\J797248.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:609 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:8 ✓
L:609 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:8 ✓
L:609 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8 after pos.:0
L:621 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:9 ✓
L:621 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:9 ✓
L:621 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9 after pos.:0 ✓
L:633 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:10 ✓
L:633 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:10 ✓
L:633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0